

PB

PCT09

## RAW SEQUENCE LISTING

DATE: 10/03/2001

PATENT APPLICATION: US/09/762,261A

TIME: 08:45:06

Input Set : A:\Hj5001us.app

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3 <110> APPLICANT: Quinnan, Gerald V.  
 4 Zhang, Peng Fei  
 6 <120> TITLE OF INVENTION: Expression and Characterization of HIV-1 Envelope  
 7 Protein Associated with a Broadly Reactive Neutralizing  
 8 Antibody Response  
 10 <130> FILE REFERENCE: 44508-5001-US  
 12 <140> CURRENT APPLICATION NUMBER: US 09/762,261A  
 13 <141> CURRENT FILING DATE: 2001-02-05  
 15 <150> PRIOR APPLICATION NUMBER: US 60/095,267  
 16 <151> PRIOR FILING DATE: 1998-08-04  
 18 <150> PRIOR APPLICATION NUMBER: PCT/US99/17596  
 19 <151> PRIOR FILING DATE: 1999-08-04  
 21 <160> NUMBER OF SEQ ID NOS: 4  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 866  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Human immunodeficiency virus type 1  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: R2 strain envelope protein (gp 160)  
 33 <400> SEQUENCE: 1  
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 35 1 5 10 15  
 37 Gly Thr Met Leu Gly Leu Leu Met Ile Cys Ser Ala Thr Glu Lys  
 38 20 25 30  
 40 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr  
 41 35 40 45  
 43 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ala  
 44 50 55 60  
 46 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro  
 47 65 70 75 80  
 49 Gln Glu Val Glu Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp Lys  
 50 85 90 95  
 52 Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp  
 53 100 105 110  
 55 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu  
 56 115 120 125  
 58 Asn Cys Thr Asp Leu Arg Asn Thr Thr Asn Thr Asn Asn Ser Thr Asp  
 59 130 135 140  
 61 Asn Asn Asn Ser Asn Ser Glu Gly Thr Ile Lys Gly Gly Glu Met Lys  
 62 145 150 155 160  
 64 Asn Cys Ser Phe Asn Ile Ala Thr Ser Ile Gly Asp Lys Met Gln Lys  
 65 165 170 175  
 67 Glu Tyr Ala Leu Leu Tyr Lys Leu Asp Ile Glu Pro Ile Asp Asn Asp  
 68 180 185 190  
 70 Asn Thr Ser Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln  
 71 195 200 205

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73 Ala Cys Pro Lys Ile Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
74      210                      215                      220
76 Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Ser Gly
77 225                      230                      235                      240
79 Lys Gly Ser Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
80      245                      250                      255
82 Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
83      260                      265                      270
85 Glu Glu Val Val Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr
86      275                      280                      285
88 Ile Ile Val Gln Leu Arg Glu Pro Val Lys Ile Asn Cys Ser Arg Pro
89      290                      295                      300
91 Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe
92 305                      310                      315                      320
94 Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn
95      325                      330                      335
97 Ile Ser Lys Thr Asn Trp Thr Asn Ala Leu Lys Gln Val Val Glu Lys
98      340                      345                      350
100 Leu Gly Glu Gln Phe Asn Lys Thr Lys Ile Val Phe Thr Asn Ser Ser
101      355                      360                      365
103 Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Ala Gly Glu
104      370                      375                      380
106 Phe Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asp Ser Ile Trp Asn Ser
107 385                      390                      395                      400
109 Glu Asn Gly Thr Trp Asn Ile Thr Arg Gly Leu Asn Asn Thr Gly Arg
110      405                      410                      415
112 Asn Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg
113      420                      425                      430
115 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Lys Gly Asn
116      435                      440                      445
118 Ile Ser Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
119      450                      455                      460
121 Gly Lys Asp Asp Asn Ser Arg Asp Gly Asn Glu Thr Phe Arg Pro Gly
122 465                      470                      475                      480
124 Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys
125      485                      490                      495
127 Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg
128      500                      505                      510
130 Arg Val Val Gln Arg Glu Glu Arg Ala Val Gly Leu Gly Ala Met Phe
131      515                      520                      525
133 Ile Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Val
134      530                      535                      540
136 Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln
137 545                      550                      555                      560
139 Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
140      565                      570                      575
142 Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val
143      580                      585                      590
145 Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser

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146          595          600          605
148 Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser
149          610          615          620
151 Lys Asn Lys Thr Leu Glu Ala Ile Trp Asn Asn Met Thr Trp Met Gln
152 625          630          635          640
154 Trp Asp Lys Glu Ile Asp Asn Tyr Thr Lys Leu Ile Tyr Ser Leu Ile
155          645          650          655
157 Glu Glu Ser Gln Ile Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu
158          660          665          670
160 Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Trp
161          675          680          685
163 Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly
164          690          695          700
166 Leu Arg Ile Val Phe Val Val Leu Ser Ile Val Asn Arg Val Arg Gln
167 705          710          715          720
169 Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Ala Pro Arg Gly
170          725          730          735
172 Pro Asp Arg Pro Glu Glu Ile Glu Glu Gly Gly Asp Arg Asp Arg
173          740          745          750
175 Asp Arg Ser Gly Leu Leu Val Asp Gly Phe Leu Thr Leu Ile Trp Val
176          755          760          765
178 Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu
179          770          775          780
181 Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp
182 785          790          795          800
184 Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu
185          805          810          815
187 Leu Lys Asn Ser Ala Val Ser Leu Phe Asn Ala Thr Ala Ile Ala Val
188          820          825          830
190 Ala Glu Gly Thr Asp Arg Val Ile Glu Val Leu Gln Arg Val Gly Arg
191          835          840          845
193 Ala Leu Leu His Ile Pro Thr Arg Ile Arg Gln Gly Leu Glu Arg Ala
194          850          855          860
196 Leu Leu
197 865

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200 &lt;210&gt; SEQ ID NO: 2

201 &lt;211&gt; LENGTH: 17

202 &lt;212&gt; TYPE: PRT

203 &lt;213&gt; ORGANISM: Human immunodeficiency virus type 1

205 &lt;220&gt; FEATURE:

206 &lt;223&gt; OTHER INFORMATION: segment of R2 strain V3 domain

208 &lt;400&gt; SEQUENCE: 2

209 Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln

210 1 5 10 15

212 Ile

216 &lt;210&gt; SEQ ID NO: 3

217 &lt;211&gt; LENGTH: 35

218 &lt;212&gt; TYPE: PRT

219 &lt;213&gt; ORGANISM: Human immunodeficiency virus type 1

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221 <220> FEATURE:  
222 <223> OTHER INFORMATION: R2 strain V3 domain  
224 <400> SEQUENCE: 3  
225 Cys Ser Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro  
226 1 5 10 15  
228 Gly Arg Ala Phe Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln  
229 20 25 30  
231 Ala His Cys  
232 35  
235 <210> SEQ ID NO: 4  
236 <211> LENGTH: 35  
237 <212> TYPE: PRT  
238 <213> ORGANISM: Human immunodeficiency virus type 1  
240 <220> FEATURE:  
241 <223> OTHER INFORMATION: V3 domain of strain 93TH966.8  
243 <400> SEQUENCE: 4  
244 Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Thr Thr Ile Gly Pro  
245 1 5 10 15  
247 Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr Gly Asn Ile Arg Lys  
248 20 25 30  
250 Ala Tyr Cys  
251 35

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/762,261A

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